

DRAWINGS

FIG. 1

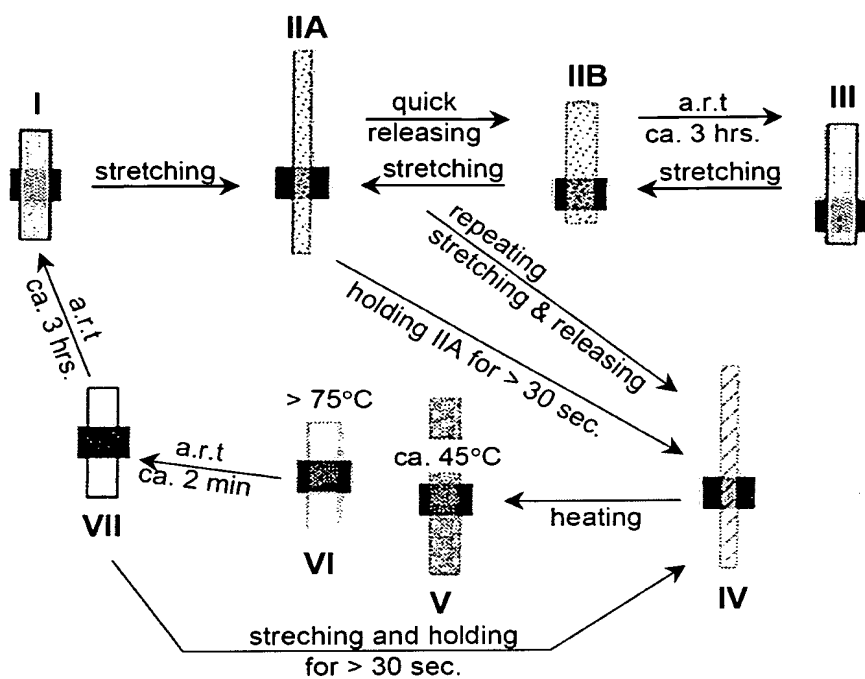
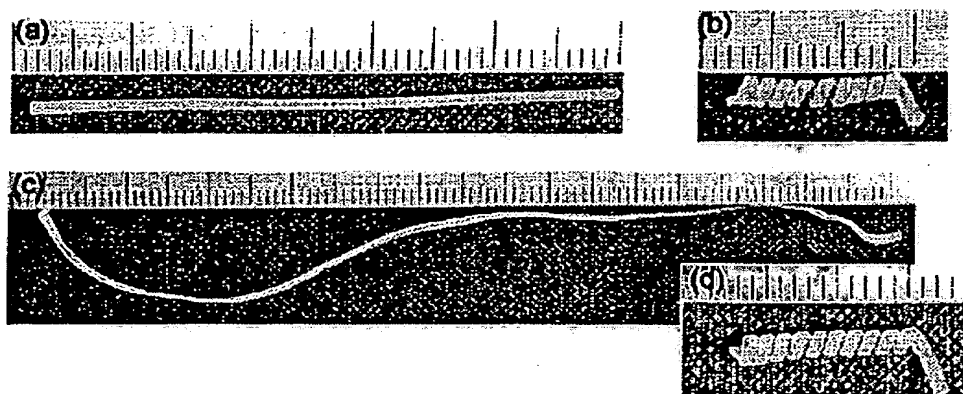


FIG. 2



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FIG. 3

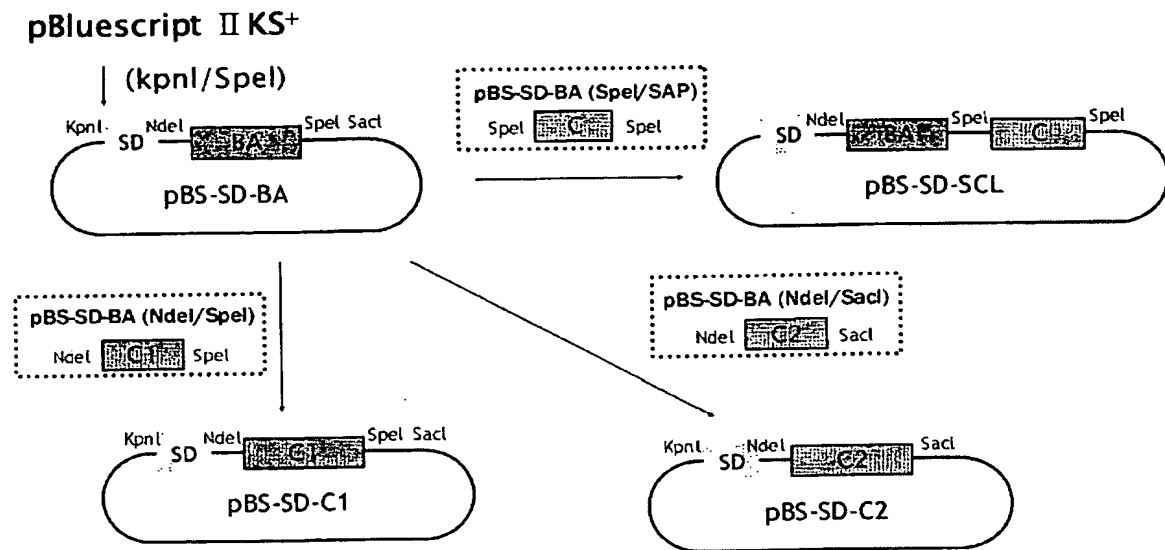
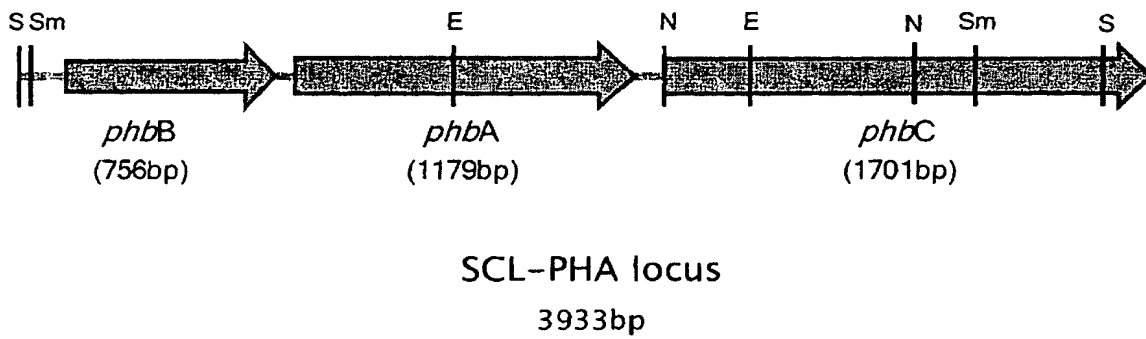


FIG. 4



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FIG. 5

phbC locus

1	GAGCTCAATG CCGCCAGGA CTGTGTGG AGGACACC GCGTCACCC GGGACATTG TTCATCCG CAAGCGGCA GAGACTGCC CGCTGTCCA AGGTCTTAT TAACAGGAA
	<i>phbB</i> →
121	Y G T A S N A A R I A L V T G G M G G I G T A I S Q R L H R D G F T V V V G TGGTAAATG GTACTGGAG CAATGCGCA CGTATAGTC TGTACACG TGTATGGC GGTATGGTA CCGGATCAG CCGAGGCTG CATCGGATG GCTTCACCT GGTGTCGCC
241	C N P Y S S R K A S W I A T Q L E A G F H F H C I D C D I T D W D S T R Q A F D TGTATCCCT ACTCAGCG CAGGCTTCC TGGATTGCA CCGAATCGA GCGGGCTTT CACTTCACCT GCATGACTG CGATCAAC GACTGGATA GCACCGGCA GGCCTTCGAC
361	M V H E T V G P I D V L V N N A G I T R D G T F R K M S P E N W K A V I D T N L ATGTGCAG AGACTGTGG CCGATCGAT GTATTGTCA ACATGCGG CATCAGCG CATCAGCTT TCGGAGAT GTCCCGGAA AACTGGAAG GCGTGATGA TACCATCTC
481	T G L F N T T K Q V I E G M L A K G W G R V I N I S S I N G Q R G Q F G Q T N Y ACCGCCTGT TCACACAC CAAGAGTC ATGAGGCA TGTGAGCA GCGCTGGGA CCGTCTCA ACATCTCTC AATCAATGC CAGCGAGCC ACTTCGGCA GACCAACTAC
601	S A X K A G I H G F S M A L A R E V S G K G V T V N T V S P G Y I K T D M T A A TCCGCGNCA AGGCTGGAT TCATGGCTC AGCATGGCT TCGCCCGGA GGTGAGTGC CCGTCAATAC GGTTCGCCCT GGTACATCA AGACCGCAT GACCGCGCG
721	I R P D I L E D M I T G I P V G R L G Q P E E I A S I V A W L A S D Q S A Y A T ATTGCGCG ACATCTCGA AGCATGATT ACTGGCATC CCGTGGCG TCTCGCGAG CCGGAGGGA TCGCTCGAT CCGTGGCTGG CTGGCTCG ATCAGTCTC CTATGGCACC
	<i>phbA</i> →
841	G A D F S V N G G M N M Q * GCGCGGACT TCTCGTGAA TCGCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT GATCGCAT
961	T A I G A F Q G S L A G T P A V E L G A T V I R R L L E Q T A L D S S Q V D E V ACCGCATCG CCGCTTTCCA GCGGAGCTG GCGGAGCTC CCGCGTGA ACTGCGGCG CCGGCTGCT CCGACAGCC GCTCTGATA GAGTCACT GGTGAGTGG
1081	I L G H V L T A G A G R I P L A R X X V I A G L P H A V P A M T L N K V C G S G ATCTCGCC AGTACTAC CCGCGTGT GGCAGATAC CCGTGGCAG GCANNGTC ATCGCGGCG ATGACCGG ATGACCGG ATGACCGG ATGACCGG ATGACCGG ATGACCGG
1201	L K A L H L G A Q A I R C G D A E V V I A G G M E N M S L S S Y V L P K A R T G CTGAAAGCC TCGACTGG CCGCCAGCC ATCGCTCTG GCGATCGGA GGTGTGATT CCGGTCGGA TGGAGACAT GAGCTGTGG TCTATGTCC TCGCCAGCC CCGCACCGC
1321	L R M G H A Q L V D S M I V D G L W D A F N D Y H M G I T A E N L V D K Y G I S CTGCGCATGG CCGAGGCA GCTGTGCA AGCATGATG TCGAGGCT GTGAGGCTC TTCAGGACT ACCATGCG GATCACTCC GAGAACCTGG TAGACAGTA CCGCATCAG
1441	R E A Q D E F A A A S Q Q K A V A A I E T G R F R D E I V P V S I P Q R K G E A CGCGAGCC AGGAGGATT CG CCGGCC TCGACAGA AGCGGTGG CCGCATGAG ACCGTCCT TCGCGAGA GATGTCTCG GTGACATTC CCGAGGCA GCGGAGGCG
1561	L S F D T D E Q P R A G T T A E S L G K L K P A F K N D G S V T A G N A S S L N CTGAGTTC ACACGAGA CCGGAGCA CCGGAGCA GCTGCGAG CCGGAGCA CCGGAGCA CCGGAGCA CCGGAGCA CCGGAGCA CCGGAGCA CCGGAGCA CCGGAGCA
1681	D G A A A V L L M S A A K A A A L G L P V L A K I A A Y A N A G V D P A I M G I GACGCGCG CCGCGTACT GCTGATGAT GGTGTGCA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA GTGTGCGA
1801	G P V S A T R S C L E K A G W S L A E L D L I E A N E A F A A Q A L A V G Q E L GGACCGGTGT CCGCCAGCC CAGTTGCTG GAGAGGCG GCTGGAGTCT GCGAGAGCT GATCTGATG AGGCGATGA AGCTTGGG GCGGAGGCC TGGCGGTGG TCAGGAGCTG

FIG. 6

1921	G W D A G R V N V N G G A I A L G H P I G A S G C R V L V S L L H E M L R R D A GGCTGGATG CTGGAGGT TACGTCAAC GGGGGGCA TGGCCTCGG CCACCCATT GGGGCTCGG GCTGGCGGT ACTGGTCAG CTGCTGATG AATGCTCAG GGGGAGCGG K G L A T L C I G G G Q G V A L A I E R *
2041	AAAAAGGCC TGCTACCT GTGTATCGT GGGGGCAGG GGGTGGCGT GGGCATCAG CGCTTAGTGA CGCTTTGGG ACTCTGCGG AGGTGCCCC CTGCACCGG AGGGCAGGC M D N G H T F A H Y W S G Q A P phbc →
2161	TGGCGCTGG GTTACGTCT GACATGATG CACCGCGGG GGGGCTTGG TTTCATATT CTRGAGAGG CCATGACA GAGACACCC TTGCTCACT ACTGCTGGG TCAGCGCGCC F I A S F V L Q Q L R L Y V A Q N T W F S G H D Q S Q W F D V P V E A L E Q L Q
2281	TTATCGCA GCTTGCTCT GCAGCACTG CGCTTATAG TGGGCAAMA TACTTGGTC ABGGGCGAG ACCAAGCA GTGTTGAC GTACTCTGG AGGGTTGGA GCACCTGAG A D Y Q Q Q W A E L G Q Q L L S C Q P F A F S D R R F A S G N W S E P L F G S L
2401	GGGACTACC AACACAGTG GCGGAACCT GGCAGCAAT TGTGAGCTG CCAGCGCTTC GCAITCAGG ATGCTGCTT CGCAGTGG AACGAGG AACGCTGTT CGGTTCCCTG A A F Y L L N S G F L L K L L E L L P I D E Q K P R Q R L R Y L I E Q A I A S
2521	GCTGCTCT ACCTGCTGAA TTGCGTTTC CTGCTGAAC TGTGGAGCT TCCTCCCATC GATGAGCA AGCCCGGCA GGGTTGGT TACTTGATG AGCAAGGAT TCGCGCAGC A P S N F L L S N P D A L Q R L V E T Q G A S L L S G L L H A S D L Q A G K L
2641	GCCCCAGTA ACTTCTGCT GAGCAACCT GATGCCCTG AACGCTAGT GGAAGCCAG GGGGCGAGC TACTAAGTGG CTTGTTGAT CTTGCCAGT ACCTGAGGC AGCCAGTTG R Q C D L G D F E V G V N L A T T P G A V V L E T P L F Q L I Q Y S P L S E T Q
2761	CGCCATGT ACTTGGGCA TTGGAAGTC GGGTGAATC TGGCAGCAC CCGTGTGCG GTGCTACTG AMAGCCTCT GTTCCAGTG ATCCAGTATT CCGGCTCAG CGAAAGCCA Y Q R P I F M V P P W I N K Y Y I L D L G P E N S L I R H L L E R G H Q V F L M
2881	TACGAGGCG CGATATTCA GTTCCGCGC TGGATCAAC ACTACTCAT CTTGACCTC GGGCGGAAA ACTCTTAAT CCGTCATCTA CTGAGCGAG GCCATCAAGT TTTTCTGATG S W R N F T Q E Q A D I T W E Q I I Q D G V I S A L R T T R A I S G E R H L N C
3001	TCCTGCGCA ACTTCACTCA GGAACAGGC GACATCACT GGGAGCAGAT CATCCAGAC GGAATGATCA GGGCGCTGG CACTACCGG GCCATCAGT GTGAGCGCA CCGTACTGT L G F C I G G T N L S C A L A V L A A R G D Q D I A S L S L F A T F L D Y L D T
3121	TTGGTTTCT GCATCGCGG CACCATGCTG AGTTGCGCTC TAGCGTCTT GGCAGCGGT GGGAGCAGG ACAATTGCG CCGTACTT TCTTGACTA CTTGATACC G P I S V F V D E Q L V A Y R E R T I G G H G G K C G L F R G E D M G N T F S L
3241	GGCGCATCA GCGTCTTCT CGATGAGCA CTGCTGCTT ACCTGAGCG CACCATCGT GGGCATGCTG GCAATGTGG CCGTTTCCG CCGTAGGACA TGGCAATAC CTTCTCCCTG L R P N E L W W N Y N V D K Y L K G Q K P L A L G L L F W N N D S T N L P G P L
3361	CTGCGGCCA ACGAGCTGT GTGAACCTAC AACGTAGACA AATATCTCA GGGCAGAG CCGCTGGCTC TGGTCTACT GTTCTGGAAC AAGCAGCA CCAATCTGCC GGGGCGCTG Y C W Y L R H T Y L Q N D L K S G E L D L C G V K L D L R A I D A P A Y I L G T
3481	TATTGCTGT ATCTGCGCA CACCTACCTG CAGAGGACC TCMAATCGG GGAATGAT CTGTGCGG TCAAGTTGGA TCTGCGGCG ATAGCCAG CAGCTACAT CTTGGGAACC H D D H I V P W R S A Y A S T E L L G G P K R F V L G A S G H I A G V I N P P D
3601	CATGAGACC ACATGCTGCC CTGGCGAGC GCCTATGCA GCAGGAATT GCTGGAGGT CCAGCGCTT TGTGCTCGG CGGCTCGG CACATCGCG GGTGATCAA CCGGCGAGT R N K R H Y W V N E H I A P V A D W L Q G A Q Q H S G S W W G D W F A W L T G
3721	AGGAACAAGC GCCATTACTG GTTCAATGAA CACATAGCG CGGTAGCTGA CGACTGGCTG CAGGAGCTC AGACGATTC CCGCAGTTGG TGGGTGACT GGTTCGCTG GTTCACCGG Y A G P R K P A I T M L G S A E Y P P L E H A P G R Y V K L *
3841	TATGCGGCC CACCAAGCC TGGCATCACT ATGCTGGCA GTGCCAGTA CCGCGGCTT GAATGTCG CAGGACCTTA TGTGAAGCTA TGA